#13

SEQUENCE LISTING

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<120> METHODS OF CONFERRING PPO-INHIBITING HERBICIDE RESISTANCE IN PLANTS BY GENE MANIPULATION

<130> 2185-156P

<140> US 09/331,723
<141> 1999-08-18

<150> PCT/US96/20415
<151> 1996-12-27

<160> 24

<170> PatentIn version 3.0

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<212> PRT
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<220>
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<220>
<221> PEPTIDE
<222> (1)..(47)
<223> product = porphyric herbicide resistance domain

<400> 1

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1               5                  10                  15
Thr Leu Ser Tyr Pro Leu Ser Ala Val Arg Glu Glu Arg Lys Ala Ser
            20                  25                  30
Asp Gly Ser Val Pro Gly Phe Gly Gln Leu His Pro Arg Thr Gln
        35                  40                  45
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<210> 2
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<212> PRT
<213> Arabidopsis thaliana

<220>
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<223> ecotype Columbia

<220>
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<222> (1)..(46)
<223> product = porphyric herbicide resistance domain

<400> 2

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
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Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
20 25 30
Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
35 40 45

<210> 3
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<212> PRT
<213> Zea mays

<220>
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<223> Strain B73 inbred

<220>
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<222> (1)..(46)
<223> product = porphyric herbicide resistance domain

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Ala Ala Asp Ala Leu Ser Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val
1 5 10 15
Thr Val Ser Tyr Pro Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp
20 25 30
Gly Glu Leu Gln Gly Phe Gly Gln Leu His Pro Arg Ser Gln
35 40 45

<210> 4
<211> 141
<212> DNA
<213> Chlamydomonas reinhardtii

<220>
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<223> Strain CC-407

<220>
<221> misc_feature
<222> (1)..(141)
<223> encodes porphyric herbicide resistance domain

<400> 4
gccgccgagg ccctgggctc cttcgactac ccgccggtgg gcgccgtgac gctgtcgtac 60
ccgctgagcg ccgtgcggga ggagcgcaag gcctcggacg ggtccgtgcc gggcttcggt 120
cagctgcacc cgcgcacgca g 141

<210> 5
<211> 138
<212> DNA
<213> Arabidopsis thaliana

<220>
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<223> ecotype Columbia

<220>
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<222> (1)..(138)
<223> encodes porphyric herbicide resistance domain

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gctgcaaatg cactctcaaa actatattac ccaccagttg cagcagtatc tatctcgtac 60
ccgaaagaag caatccgaac agaatgtttg atagatggtg aactaaaggg ttttgggcaa 120
ttgcatccac gcacgcaa 138

<210> 6
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<212> DNA
<213> Zea mays

<220>
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<220>
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<222> (1)..(138)
<223> encodes porphyric herbicide resistance domain

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ccaaaggaag caattagaaa agaatgctta attgatgggg aactccaggg ctttggccag 120
ttgcatccac gtagtcaa 138

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<222> (1)..(36)
<223> Oligonucleotide primer for Arabidopsis thaliana

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ctatattacc caccaatggc agcagtatct atctcg 36

<210> 8
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
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<222> (1)..(38)
<223> Oligonucleotide primer for Zea mays

<400> 8
gattctatta tccaccgatg gctgctgtaa ctgtttcg 38

<210> 9
<211> 26
<212> DNA

<213> Artificial Sequence

<220>
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<222> (1)..(26)
<223> Oligonucleotide primer common to both of A. thaliana and Z. mays porphyric herbicide resistance domain of PP

<220>
<221> misc_feature
<222> (1)..(26)
<223> "n" residues can be inosine in addition to G, A, T or C; "k" at position 1 is equal to G or T; "y" at positions 3 and 6 is equal to C or T; "s" at positions 17 and 26 is equal to C or G; and "w" at position 25 is equal to A or T

<400> 9
kaytayccnc cnatggsngc ngtnws 26

<210> 10
<211> 2573
<212> DNA
<213> Chlamydomonas reinhardtii

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<221> misc_feature
<223> Strain RS-3

<220>
<221> misc_feature
<222> (1)..(2573)
<223> encodes protoporphyrinogen oxidase

<400> 10
ctcgagagcg ttggaggaaa tccgtttggc acctgttccg gcttctttgt gtgcacggcc 60
acgtcccccc ttcctgctac ccgctccccc ccggctttac tgccccttcc actcctcggc 120
tccatcccga ttccatccgc tcctcctccc ccacctagac tgtctaccgt ctaccagttt 180
cttgggcaat cattaacgta accccgcctc cctgcgcctg cccctccctc cctctccccc 240
ccgcacagcc cgccgccgcc gaggccctgg gctccttcga ctacccgccg atgggcgccg 300
tgacgctgtc gtacccgctg agcgccgtgc gggaggagcg caaggcctcg gacgggtccg 360
tgccgggctt cggtcagctg cacccgcgca cgcaggtggg caagtgcgcg cgtgttgcgg 420
gcggtgtgtt gcggagggga gggtggtggg ggttgggggt gggggtgggg gggattgggg 480
cgctgggtcg tatcccgcgg ttgtatcctc gcgctcccct catccattcc ccccttcaac 540
aacacacacg ggcgcacacg caccctcttt gcgcttactt tgtctggtgc tccttaacac 600
actcttcgct tcattttggt gtcttctaac acacacactt gtccacacac agggcatcac 660
cactctgggc accatctaca gctccagcct gttccccggc cgcgcgcccg agggccacat 720
gctgctgctc aactacatcg gcggcaccac caaccgcggc atcgtcaacc agaccaccga 780
gcagctggtg gagcaggtgt gtgtgtgggg gggtgggggg ggggcagtgg atttttgggc 840
tgagcccccc gagcaaagcg atccaggggg ggcgaagccc cccaggattg cccctgtccg 900
tgcgtgcgtg tgtgcctgtg tcgacaaaaa gtaccgtact ggcacaaacc gcgagtgcca 960
cgtattatta attgcaatta cctattgtag aaaaatagac ggcagggaaa actcggccgg 1020
agcgagaagc gacctcgtga gtccatggac atcttgactt tcttcagttc gcgagtatag 1080
ctctcggccc ctaaatatct tacatccatg tatcaaaaca tgtcgacgac aagcgtcttg 1140
gggcaagaat gtcgaaattg tttgcaacag ccaaaccatg cgtccccgag ccttacatgt 1200
gtcgcggccc gggatcccgc gcccgagccc ggctagccct ttgcggtgct tgagtgggat 1260
gtgggtgagg tgcatttggg atatcatgga ccgtgaagtg gcgtgggtaa ggtggcgtgg 1320
cgtggcgggg acagggcatg tcggtgcctc ggcacagcgt tggcctagtg gccagtcccg 1380
ctggatgggc ttgcaagggt gctgttcatg tcgccggtgc ccatcgtcac atccccttgc 1440
gctacatggg gctcagccca ttttccagct gtacaaagct gacacccctt gttgtgtggc 1500

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gtcttggacc cgtgttgctt cggagctggc cagaaccccc tgtgggcaca cacacgcaca   1560
cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca   1620
cacacacaca cacacacaca cacacacaca cacacacaca cacattttcg tcctgcagcc   1680
ccgaaccccg ccgcccgttc cacgtcttcc acctgccgca ccccccccgc tgccgcacgc   1740
ctgctctcac cgcctctccc cccaccccat ctccctgcag gtggacaagg acctgcgcaa   1800
catggtcatc aagcccgacg cgcccaagcc ccgtgtggtg ggcgtgcgcg tgtggccgcg   1860
cgccatcccg caggtgtgag ggcgcagcag ccggagggat gggctagatc ctagtttctc   1920
aaagagctct acagccctat aacctcgacc tgcgaccttc gacctgataa cctggctgcc   1980
ccctcccaac ctagccacct ctccccggat ttgggttcac tcggttgact tgcttttggg   2040
ttctggaatc aacttcacct gttgtatact ttgctgcact tctctgtacc actctttgca   2100
ttaggttcgg tttagtttgg gctgcatgtg taacccctcc tccccgccct gccacctgca   2160
gttcaacctg ggccacctgg agcagctgga caaggcgcgc aaggcgctgg acgcggcggg   2220
gctgcagggc gtgcacctgg ggggcaacta cgtcagcggt gagcgcgtgg gcagcagcag   2280
cagcaggaag aggggagggg aggggagggg agggtacaag gaggaggttg agcaggaggt   2340
ggtgctaagg cgcaaagcaa ggcggtgttg tatcctcatt gactgaaacc gggaaaccca   2400
gcatgaacaa gaggtcaggg gactgcaagg agcggaggct acatgtatga ctacccccga   2460
cgcgggcgat gattccttga ctattgggac ctatttcgtt gggctcgggc acatgacccc   2520
cctggcccct tcgctgtatg gtgcccagcc gcccagccgc cccccgccca cac          2573
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<210> 11
<211> 1704
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<223> ecotype Columbia

<220>
<221> CDS
<222> (16)..(1629)
<223> product = protoporphyrinogen oxidase

<400> 11

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ttctctgcga tttcc atg gag tta tct ctt ctc cgt ccg acg act caa tcg      51
                 Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser
                 1               5                  10
ctt ctt ccg tcg ttt tcg aag ccc aat ctc cga tta aat gtt tat aag       99
Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys
        15                  20                  25
cct ctt aga ctc cgt tgt tca gtg gcc ggt gga cca acc gtc gga tct      147
Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser
    30                  35                  40
tca aaa atc gaa ggc gga gga ggc acc acc atc acg acg gat tgt gtg      195
Ser Lys Ile Glu Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val
45                  50                  55                  60
att gtc ggc gga ggt att agt ggt ctt tgc atc gct cag gcg ctt gct      243
Ile Val Gly Gly Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala
                65                  70                  75
act aag cat cct gat gct gct ccg aat tta att gtg acc gag gct aag      291
Thr Lys His Pro Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys
            80                  85                  90
gat cgt gtt gga ggc aac att atc act cgt gaa gag aat ggt ttt ctc      339
Asp Arg Val Gly Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu
        95                  100                 105
tgg gaa gaa ggt ccc aat agt ttt caa ccg tct gat cct atg ctc act      387
Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr
    110                 115                 120
atg gtg gta gat agt ggt ttg aag gat gat ttg gtg ttg gga gat cct      435
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Met Val Val Asp Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro
125                 130                 135                 140
act gcg cca agg ttt gtg ttg tgg aat ggg aaa ttg agg ccg gtt cca      483
Thr Ala Pro Arg Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro
                145                 150                 155
tcg aag cta aca gac tta ccg ttc ttt gat ttg atg agt att ggt ggg      531
Ser Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly
            160                 165                 170
aag att aga gct ggt ttt ggt gca ctt ggc att cga ccg tca cct cca      579
Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro
        175                 180                 185
ggt cgt gaa gaa tct gtg gag gag ttt gta cgg cgt aac ctc ggt gat      627
Gly Arg Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp
    190                 195                 200
gag gtt ttt gag cgc ctg att gaa ccg ttt tgt tca ggt gtt tat gct      675
Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala
205                 210                 215                 220
ggt gat cct tca aaa ctg agc atg aaa gca gcg ttt ggg aag gtt tgg      723
Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp
                225                 230                 235
aaa cta gag caa aat ggt gga agc ata ata ggt ggt act ttt aag gca      771
Lys Leu Glu Gln Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala
            240                 245                 250
att cag gag agg aaa aac gct ccc aag gca gaa cga gac ccg cgc ctg      819
Ile Gln Glu Arg Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu
        255                 260                 265
cca aaa cca cag ggc caa aca gtt ggt tct ttc agg aag gga ctt cga      867
Pro Lys Pro Gln Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg
    270                 275                 280
atg ttg cca gaa gca ata tct gca aga tta ggt agc aaa gtt aag ttg      915
Met Leu Pro Glu Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu
285                 290                 295                 300
tct tgg aag ctc tca ggt atc act aag ctg gag agc gga gga tac aac      963
Ser Trp Lys Leu Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn
                305                 310                 315
tta aca tat gag act cca gat ggt tta gtt tcc gtg cag agc aaa agt     1011
Leu Thr Tyr Glu Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser
            320                 325                 330
gtt gta atg acg gtg cca tct cat gtt gca agt ggt ctc ttg cgc cct     1059
Val Val Met Thr Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro
        335                 340                 345
ctt tct gaa tct gct gca aat gca ctc tca aaa cta tat tac cca cca     1107
Leu Ser Glu Ser Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro
    350                 355                 360
gtt gca gca gta tct atc tcg tac ccg aaa gaa gca atc cga aca gaa     1155
Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu
365                 370                 375                 380
tgt ttg ata gat ggt gaa cta aag ggt ttt ggg caa ttg cat cca cgc     1203
Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg
                385                 390                 395
acg caa gga gtt gaa aca tta gga act atc tac agc tcc tca ctc ttt     1251
Thr Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe
            400                 405                 410
cca aat cgc gca ccg ccc gga aga att ttg ctg ttg aac tac att ggc     1299
Pro Asn Arg Ala Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly
        415                 420                 425
ggg tct aca aac acc gga att ctg tcc aag tct gaa ggt gag tta gtg     1347
Gly Ser Thr Asn Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val
    430                 435                 440
gaa gca gtt gac aga gat ttg agg aaa atg cta att aag cct aat tcg     1395
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Glu Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser
445                 450                 455                 460
acc gat cca ctt aaa tta gga gtt agg gta tgg cct caa gcc att cct     1443
Thr Asp Pro Leu Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro
                465                 470                 475
cag ttt cta gtt ggt cac ttt gat atc ctt gac acg gct aaa tca tct     1491
Gln Phe Leu Val Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser
            480                 485                 490
cta acg tct tcg ggc tac gaa ggg cta ttt ttg ggt ggc aat tac gtc     1539
Leu Thr Ser Ser Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val
        495                 500                 505
gct ggt gta gcc tta ggc cgg tgt gta gaa ggc gca tat gaa acc gcg     1587
Ala Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala
    510                 515                 520
att gag gtc aac aac ttc atg tca cgg tac gct tac aag taa             1629
Ile Glu Val Asn Asn Phe Met Ser Arg Tyr Ala Tyr Lys
525                 530                 535
atgtaaaaca ttaaatctcc cagcttgcgt gagttttatt aaatattttg agatatccaa   1689
aaaaaaaaaa aaaaa                                                    1704
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<210> 12
<211> 537
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<223> ecotype Columbia

<400> 12

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Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys Pro Leu Arg Leu
            20                  25                  30

Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser Ser Lys Ile Glu
        35                  40                  45

Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val Ile Val Gly Gly
    50                  55                  60

Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala Thr Lys His Pro
65                  70                  75                  80

Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys Asp Arg Val Gly
                85                  90                  95

Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu Trp Glu Glu Gly
            100                 105                 110

Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Val Val Asp
        115                 120                 125

Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Thr Ala Pro Arg
    130                 135                 140

Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr
145                 150                 155                 160
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Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala
165 170 175

Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu
180 185 190

Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu
195 200 205

Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser
210 215 220

Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Gln
225 230 235 240

Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg
245 250 255

Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln
260 265 270

Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu
275 280 285

Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu
290 295 300

Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu
305 310 315 320

Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr
325 330 335

Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser
340 345 350

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
355 360 365

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
370 375 380

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val
385 390 395 400

Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala
405 410 415

Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn
420 425 430

Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp
435 440 445

Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu
450 455 460

Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val
465 470 475 480

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Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser
                485                 490                 495

Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala
            500                 505                 510

Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala Ile Glu Val Asn
        515                 520                 525

Asn Phe Met Ser Arg Tyr Ala Tyr Lys
    530                 535


<210>  13
<211>  1698
<212>  DNA
<213>  Zea mays

<220>
<221>  misc_feature
<223>  Strain B73 inbred

<220>
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<222>  (2)..(1453)
<223>  product = protoporphyrinogen oxidase

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  Asn Ser Ala Asp Cys Val Val Val Gly Gly Gly Ile Ser Gly Leu Cys
  1               5                  10                  15
acc gcg cag gcg ctg gcc acg cgg cac ggc gtc ggg gac gtg ctt gtc      97
Thr Ala Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu Val
            20                  25                  30
acg gag gcc cgc gcc cgc ccc ggc ggc aac att acc acc gtc gag cgc     145
Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg
        35                  40                  45
ccc gag gaa ggg tac ctc tgg gag gag ggt ccc aac agc ttc cag ccc     193
Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro
    50                  55                  60
tcc gac ccc gtt ctc acc atg gcc gtg gac agc gga ctg aag gat gac     241
Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp
65                  70                  75                  80
ttg gtt ttt ggg gac cca aac gcg ccg cgt ttc gtg ctg tgg gag ggg     289
Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly
                85                  90                  95
aag ctg agg ccc gtg cca tcc aag ccc gcc gac ctc ccg ttc ttc gat     337
Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp
            100                 105                 110
ctc atg agc atc cca ggg aag ctc agg gcc ggt cta ggc gcg ctt ggc     385
Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly
        115                 120                 125
atc cgc ccg cct cct cca ggc cgc gaa gag tca gtg gag gag ttc gtg     433
Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val
    130                 135                 140
cgc cgc aac ctc ggt gct gag gtc ttt gag cgc ctc att gag cct ttc     481
Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe
145                 150                 155                 160
tgc tca ggt gtc tat gct ggt gat cct tct aag ctc agc atg aag gct     529
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Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala
                165                 170                 175
gca ttt ggg aag gtt tgg cgg ttg gaa gaa act gga ggt agt att att      577
Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile
            180                 185                 190
ggt gga acc atc aag aca att cag gag agg agc aag aat cca aaa cca      625
Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro
        195                 200                 205
ccg agg gat gcc cgc ctt ccg aag cca aaa ggg cag aca gtt gca tct      673
Pro Arg Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser
    210                 215                 220
ttc agg aag ggt ctt gcc atg ctt cca aat gcc att aca tcc agc ttg      721
Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu
225                 230                 235                 240
ggt agt aaa gtc aaa cta tca tgg aaa ctc acg agc att aca aaa tca      769
Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser
                245                 250                 255
gat gac aag gga tat gtt ttg gag tat gaa acg cca gaa ggg gtt gtt      817
Asp Asp Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val
            260                 265                 270
tcg gtg cag gct aaa agt gtt atc atg act att cca tca tat gtt gct      865
Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala
        275                 280                 285
agc aac att ttg cgt cca ctt tca agc gat gct gca gat gct cta tca      913
Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser
    290                 295                 300
aga ttc tat tat cca ccg gtt gct gct gta act gtt tcg tat cca aag      961
Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys
305                 310                 315                 320
gaa gca att aga aaa gaa tgc tta att gat ggg gaa ctc cag ggc ttt     1009
Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe
                325                 330                 335
ggc cag ttg cat cca cgt agt caa gga gtt gag aca tta gga aca ata     1057
Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile
            340                 345                 350
tac agt tcc tca ctc ttt cca aat cgt gct cct gac ggt agg gtg tta     1105
Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu
        355                 360                 365
ctt cta aac tac ata gga ggt gct aca aac aca gga att gtt tcc aag     1153
Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys
    370                 375                 380
act gaa agt gag ctg gtc gaa gca gtt gac cgt gac ctc cga aaa atg     1201
Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met
385                 390                 395                 400
ctt ata aat tct aca gca gtg gac cct tta gtc ctt ggt gtt cga gtt     1249
Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val
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tgg cca caa gcc ata cct cag ttc ctg gta gga cat ctt gat ctt ctg     1297
Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu
            420                 425                 430
gaa gcc gca aaa gct gcc ctg gac cga ggt ggc tac gat ggg ctg ttc     1345
Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe
        435                 440                 445
cta gga ggg aac tat gtt gca gga gtt gcc ctg ggc aga tgc gtt gag     1393
Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu
    450                 455                 460
ggc gcg tat gaa agt gcc tcg caa ata tct gac ttc ttg acc aag tat     1441
Gly Ala Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr
465                 470                 475                 480
gcc tac aag tga tgaaagaagt ggagcgctac ttgccaatcg tttatgttgc         1493
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Ala Tyr Lys

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Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg
35 40 45

Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro
50 55 60

Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp
65 70 75 80

Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly
85 90 95

Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp
100 105 110

Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly
115 120 125

Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val
130 135 140

Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe
145 150 155 160

Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala
165 170 175

Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile
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Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro
195 200 205

Pro Arg Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser
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Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu
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Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser
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Asp Asp Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val
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Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala
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Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser
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Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys
305                 310                 315                 320

Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe
                325                 330                 335

Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile
            340                 345                 350

Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu
        355                 360                 365

Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys
    370                 375                 380

Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met
385                 390                 395                 400

Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val
                405                 410                 415

Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu
            420                 425                 430

Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe
        435                 440                 445

Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu
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Gly Ala Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr
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Ala Tyr Lys
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<222> (1)..(18)

<223> Oligonucleotide primer 1A for Chlamydomonas reinhardtii

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<210> 16
<211> 19
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<222> (1)..(19)
<223> Oligonucleotide primer 1B for Chlamydomonas reinhardtii

<400> 16
atacaaccgc gggatacga 19

<210> 17
<211> 17
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<222> (1)..(17)
<223> Oligonucleotide primer 2A for Chlamydomonas reinhardtii

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<223> Oligonucleotide primer 2B for Chlamydomonas reinhardtii

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<223> encodes protoporphyrinogen oxidase

<400> 19

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<220>
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<210> 21
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<223> Oligonucleotide primer 3B for Chlamydomonas reinhardtii

<400> 21
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<210> 22
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<400> 22
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<223> Oligonucleotide primer 4B for Chlamydomonas reinhardtii

<400> 23
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<210> 24
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<212> DNA
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